QMEAN Qualitative Model Energy ANalysis

CAMEO evaluation   Help   Examples ▾

pembrolizumab-abb2 (created 2025-11-03T19:58:18)   ✖

pembrolizumab-abb2 (Created: 5 minutes ago) Project Archive ⬇ Delete ✖

Total model count : 1.

Uploaded Structure:	pembrolizumab_abb2.pdb 📄
Method:	QMEANDisCo
QMEAN Version:	4.5.0
SMTL Version:	2025-10-29
SEQRES:	Not specified - sequence was extracted from coordinates.
Results:	JSON 📄

Quality for pembrolizumab_abb2.pdb

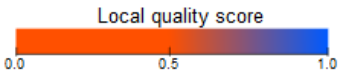Downloads ▾

Local Quality Estimate
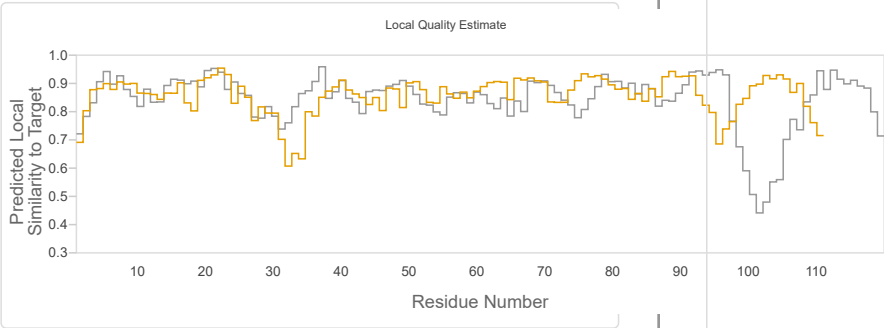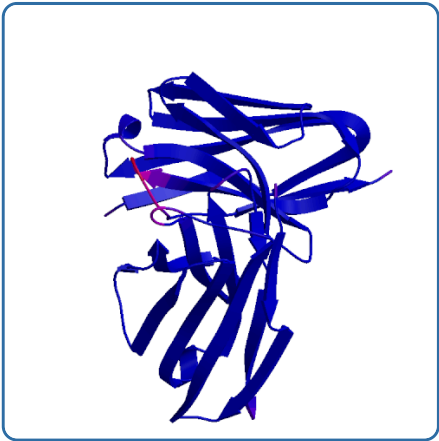
Compare ☐

QMEANDisCo Global: 0.85 ± 0.06 ❷

⚠ During preprocessing, 346 atoms were removed .

```
removing atoms with zero occupancy
 --> removed 0 atoms with zero occupancy
removing hydrogen atoms
 --> removed 346 hydrogen atoms
```

❷ **Sequence colored by local quality:**

Local quality score

0.0   0.5   1.0

H: QVQLVQSGVEVKKPGASVKVSCKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNFNEKFKNRVTLTTDSSTTTAYM

H: YRFDMGFDYWGQGTTVTVSS

L: EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESGVPARFSGSGSGTDFTLTISS

L: TFGGGTKVEIK

Reference for the QMEAN scoring function:
[1] Benkert P, Biasini M, Schwede T *Toward the estimation of the absolute quality of individual protein structure models.*
Bioinformatics 27, 343-350. (2011) 📖 21134891 🔶 10.1093/bioinformatics/btq662

Reference for the QMEANDisCo scoring function:
[2] Studer G, Rempfer C, Waterhouse AM, Gumienny R, Haas J, Schwede T *QMEANDisCo - distance constraints applied on model quality estimation.*
Bioinformatics 36, 1765-1771. (2020) 📖 31697312 🔶 10.1093/bioinformatics/btz828

Reference for the QMEANBrane scoring function:
[3] Studer G, Biasini M, Schwede T *Assessing the local structural quality of transmembrane protein models using statistical potentials (QMEANBrane).*
Bioinformatics 30, i505–i511. (2014) 📖 25161240 🔶 10.1093/bioinformatics/btu457